

# SEQUENCE LISTING

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 DIJKHUIZEN, LUBBERT  
 RAHAOUI, HAKIM

<120> NOVEL FRUCTOSYLTRANSFERASES

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<151> 2001-11-29

<150> 09/604,958

<151> 2000-06-28

<150> EPO 00201872.9

<151> 2000-05-25

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<170> PatentIn Ver. 2.1

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<213> Lactobacillus reuteri

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<212> DNA

<213> *Lactobacillus reuteri*

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<213> *Lactobacillus reuteri*

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<212> DNA

<213> Lactobacillus reuteri

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Ser	Ala	Ala	Leu	Pro	Gly	Glu	Arg	Asp	Lys	Pro	Val	Asp	Trp	Asp	Leu	
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Ile	Gly	Tyr	Gly	Leu	Lys	Pro	His	Asp	Pro	Ala	Thr	Pro	Asn	Asp	Pro	
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gaa	acg	cca	act	aca	cca	gaa	acc	cct	gag	aca	cct	aat	act	ccc	aaa	2212
Glu	Thr	Pro	Thr	Thr	Pro	Glu	Thr	Pro	Glu	Thr	Pro	Asn	Thr	Pro	Lys	
			720					725				730				
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Thr	Pro	Lys	Thr	Pro	Glu	Asn	Pro	Gly	Thr	Pro	Gln	Thr	Pro	Asn	Thr	
		735					740				745					
cct	aat	act	ccg	gaa	att	cct	tta	act	cca	gaa	acg	cct	aag	caa	cct	2308
Pro	Asn	Thr	Pro	Glu	Ile	Pro	Leu	Thr	Pro	Glu	Thr	Pro	Lys	Gln	Pro	
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gaa	acc	caa	act	aat	aat	cgt	ttg	cca	caa	act	gga	aat	aat	gcc	aat	2356
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Lys Ala Met Ile Gly Leu Gly Met Gly Thr Leu Leu Ser Met Phe Gly				
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Leu Ala Glu Ile Asn Lys Arg Arg Phe Asn				
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Glu Val Glu

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Met Tyr Lys Val Gly Lys Asn Trp Ala Val Ala	
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Thr Leu Val Ser Ala Ser Ile Leu Met Gly Gly Val Val Thr Ala His	
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Ala Asp Gln Val Glu Ser Asn Asn Tyr Asn Gly Val Ala Glu Val Asn	
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act gaa cgt caa gct aat ggt caa att ggc gta gat gga aaa att att	1396
Thr Glu Arg Gln Ala Asn Gly Gln Ile Gly Val Asp Gly Lys Ile Ile	
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agt gct aac agt aat aca acc agt ggc tcg aca aat caa gaa tca tct	1444
Ser Ala Asn Ser Asn Thr Thr Ser Gly Ser Thr Asn Gln Glu Ser Ser	
60 65 70 75	
gct act aac aat act gaa aat gct gtt gtt aat gaa agc aaa aat act	1492
Ala Thr Asn Asn Thr Glu Asn Ala Val Val Asn Glu Ser Lys Asn Thr	
80 85 90	
aac aat act gaa aat gct gtt gtt aat gaa aac aaa aat act aac aat	1540
Asn Asn Thr Glu Asn Ala Val Val Asn Glu Asn Lys Asn Thr Asn Asn	
95 100 105	
act gaa aat gct gtt gtt aat gaa aac aaa aat act aac aac aca gaa	1588
Thr Glu Asn Ala Val Val Asn Glu Asn Lys Asn Thr Asn Asn Thr Glu	
110 115 120	
aac gat aat agt caa tta aag tta act aat aat gaa caa cca tca gcc	1636
Asn Asp Asn Ser Gln Leu Lys Leu Thr Asn Asn Glu Gln Pro Ser Ala	
125 130 135	
gct act caa gca aac ttg aag aag cta aat cct caa gct gct aag gct	1684
Ala Thr Gln Ala Asn Leu Lys Lys Leu Asn Pro Gln Ala Ala Lys Ala	
140 145 150 155	
gtt caa aat gcc aag att gat gcc ggt agt tta aca gat gat caa att	1732
Val Gln Asn Ala Lys Ile Asp Ala Gly Ser Leu Thr Asp Asp Gln Ile	

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Asn	Glu	Leu	Asn	Lys	Ile	Asn	Phe	Ser	Lys	Ser	Ala	Glu	Lys	Gly	Ala					
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aaa	ttg	acc	ttt	aag	gac	tta	gag	ggg	att	ggg	aat	gct	att	gtt	aag	1828				
Lys	Leu	Thr	Phe	Lys	Asp	Leu	Glu	Gly	Ile	Gly	Asn	Ala	Ile	Val	Lys					
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caa	gat	cca	caa	tat	gct	att	cct	tat	tct	aat	gct	aag	gaa	atc	aag	1876				
Gln	Asp	Pro	Gln	Tyr	Ala	Ile	Pro	Tyr	Ser	Asn	Ala	Lys	Glu	Ile	Lys					
	205					210					215									
aat	atg	cct	gca	aca	tac	act	gta	gat	gcc	caa	aca	ggg	aag	atg	gct	1924				
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220					225				230						235					
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His	Leu	Asp	Val	Trp	Asp	Ser	Trp	Pro	Val	Gln	Asp	Pro	Val	Thr	Gly					
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tat	gta	tct	aat	tac	atg	ggg	tat	caa	cta	gtt	att	gct	atg	atg	ggg	2020				
Tyr	Val	Ser	Asn	Tyr	Met	Gly	Tyr	Gln	Leu	Val	Ile	Ala	Met	Met	Gly					
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Lys	Tyr	Gly	Asp	Asn	Asp	Phe	Ser	His	Trp	Arg	Asn	Ala	Gly	Ser	Ile					
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Thr	Ser	Asp	Tyr	Lys	Leu	Asn	Asp	Gln	Arg	Leu	Ala	Thr	Ala	Thr	Leu					
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Tyr	Gln	Val	Leu	Phe	Glu	Gly	Asp	Gly	Phe	His	Tyr	Gln	Thr	Tyr	Glu					
	365					370					375									
caa	ttc	gca	aac	ggc	aaa	gat	cgt	gaa	aat	gat	gat	tac	tgc	tta	cgt	2404				
Gln	Phe	Ala	Asn	Gly	Lys	Asp	Arg	Glu	Asn	Asp	Asp	Tyr	Cys	Leu	Arg					
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gac	cca	cac	gtt	gtt	caa	tta	gaa	aat	ggg	gat	cgt	tat	ctt	gta	ttc	2452				
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415 420 425	
aat tgg gct aac tat ggt ggc gat gat gcc ttc aat att aag agt tcc	2548
Asn Trp Ala Asn Tyr Gly Gly Asp Asp Ala Phe Asn Ile Lys Ser Ser	
430 435 440	
ttc aag ctt ttg aat aat aag aag gat cgt gaa ttg gct ggt tta gct	2596
Phe Lys Leu Leu Asn Asn Lys Lys Asp Arg Glu Leu Ala Gly Leu Ala	
445 450 455	
aat ggt gca ctt ggt atc tta aag ctc act aac aat caa agt aag cca	2644
Asn Gly Ala Leu Gly Ile Leu Lys Leu Thr Asn Asn Gln Ser Lys Pro	
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aag gtt gaa gaa gta tac tca cca ttg gta tct act ttg atg gct tgc	2692
Lys Val Glu Glu Val Tyr Ser Pro Leu Val Ser Thr Leu Met Ala Cys	
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495 500 505	
act cgt gta agt cgt ggt tcc gat cgt gaa tta acc gct aag gat aac	2788
Thr Arg Val Ser Arg Gly Ser Asp Arg Glu Leu Thr Ala Lys Asp Asn	
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Thr Ile Val Gly Asp Asn Val Ala Met Ile Gly Tyr Val Ser Asp Ser	
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Leu Met Gly Lys Tyr Lys Pro Leu Asn Asn Ser Gly Val Val Leu Thr	
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Val Pro Val Ala Gly His Pro Asp Gln Val Leu Ile Thr Ser Tyr Met	
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Ser Asn Lys Asp Phe Ala Ser Gly Glu Gly Asn Tyr Ala Thr Trp Ala	
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Pro Ser Phe Leu Val Gln Ile Asn Pro Asp Asp Thr Thr Thr Val Leu	
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gca cgt gca act aac caa ggt gac tgg gtg tgg gac gac tct agt cgg	3124
Ala Arg Ala Thr Asn Gln Gly Asp Trp Val Trp Asp Asp Ser Ser Arg	
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Asn Asp Asn Met Leu Gly Val Leu Lys Glu Gly Ala Ala Asn Ser Ala	
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aga agt cct ggc tta ggc tta aag cct cat caa cca gtt caa cca aag	3268
Arg Ser Pro Gly Leu Gly Leu Lys Pro His Gln Pro Val Gln Pro Lys	
670 675 680	
att gat caa cct gat caa caa cct tct ggt caa aac act aag aat gtc	3316
Ile Asp Gln Pro Asp Gln Gln Pro Ser Gly Gln Asn Thr Lys Asn Val	
685 690 695	
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Thr Pro Gly Asn Gly Asp Lys Pro Ala Gly Lys Ala Thr Pro Asp Asn	
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735 740 745	
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Gly Asn Glu Lys Gln Gly Lys Asn Thr Asp Ala Lys Gln Leu Pro Gln	
750 755 760	
aca ggt aat aag tct ggt tta gca gga ctt tac gct ggt tca tta ctt	3556
Thr Gly Asn Lys Ser Gly Leu Ala Gly Leu Tyr Ala Gly Ser Leu Leu	
765 770 775	
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Asn Gly Gln Ile Gly Val Asp Gly Lys Ile Ile Ser Ala Asn Ser Asn  
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65 70 75 80  
Glu Asn Ala Val Val Asn Glu Ser Lys Asn Thr Asn Asn Thr Glu Asn  
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Ile Asp Ala Gly Ser Leu Thr Asp Asp Gln Ile Asn Glu Leu Asn Lys  
165 170 175

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Ile	Leu	Lys	Leu	Thr	Asn	Asn	Gln	Ser	Lys	Pro	Lys	Val	Glu	Glu	Val		
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Tyr	Ser	Pro	Leu	Val	Ser	Thr	Leu	Met	Ala	Cys	Asp	Glu	Val	Xaa	Xaa		
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Lys	Leu	Gly	Asp	Lys	Tyr	Tyr	Leu	Phe	Ser	Val	Thr	Arg	Val	Ser	Arg		



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Gly	Ser	Asp	Arg	Glu	Leu	Thr	Ala	Lys	Asp	Asn	Thr	Ile	Val	Gly	Asp	
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Asn	Val	Ala	Met	Ile	Gly	Tyr	Val	Ser	Asp	Ser	Leu	Met	Gly	Lys	Tyr	
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Lys	Pro	Leu	Asn	Asn	Ser	Gly	Val	Val	Leu	Thr	Ala	Ser	Val	Pro	Ala	
545					550					555					560	
Asn	Trp	Arg	Thr	Ala	Thr	Tyr	Ser	Tyr	Tyr	Ala	Val	Pro	Val	Ala	Gly	
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His	Pro	Asp	Gln	Val	Leu	Ile	Thr	Ser	Tyr	Met	Ser	Asn	Lys	Asp	Phe	
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Ala	Ser	Gly	Glu	Gly	Asn	Tyr	Ala	Thr	Trp	Ala	Pro	Ser	Phe	Leu	Val	
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610					615					620						
Gln	Gly	Asp	Trp	Val	Trp	Asp	Asp	Ser	Ser	Arg	Asn	Asp	Asn	Met	Leu	
625					630					635					640	
Gly	Val	Leu	Lys	Glu	Gly	Ala	Ala	Asn	Ser	Ala	Ala	Leu	Pro	Gly	Glu	
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Trp	Gly	Lys	Pro	Val	Asp	Trp	Ser	Leu	Ile	Asn	Arg	Ser	Pro	Gly	Leu	
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Gly	Leu	Lys	Pro	His	Gln	Pro	Val	Gln	Pro	Lys	Ile	Asp	Gln	Pro	Asp	
675					680					685						
Gln	Gln	Pro	Ser	Gly	Gln	Asn	Thr	Lys	Asn	Val	Thr	Pro	Gly	Asn	Gly	
690					695					700						
Asp	Lys	Pro	Ala	Gly	Lys	Ala	Thr	Pro	Asp	Asn	Thr	Asn	Ile	Asp	Pro	
705					710					715					720	
Ser	Ala	Gln	Pro	Ser	Gly	Gln	Asn	Thr	Asn	Ile	Asp	Pro	Ser	Ala	Gln	
725					730					735						
Xaa	Ser	Gly	Gln	Asn	Thr	Lys	Asn	Val	Thr	Pro	Gly	Asn	Glu	Lys	Gln	
740					745					750						
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<213> Streptococcus salivarius

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